Analyzing Risk Factors for Diabetes By Isaiah Dominguez

In this project, we explore a real-world clinical dataset to identify potential risk factors associated with diabetes. Using data analysis and visualization, we examine patterns in BMI, glucose, insulin, and family history, and engineer new insights from the data. This analysis demonstrates the application of core data science skills in a health context.

First we load the dataset,libraries, and tools we are going to use.

In [2]:
```
!pip install pandas matplotlib seaborn numpy
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
df  =  pd.read_csv("C:/Users/Bigza/Downloads/archive/diabetes.csv")
df.head()
```

```
Requirement already satisfied: pandas in c:\users\bigza\onedrive\documents\anaconda
\lib\site-packages (2.1.4)
Requirement already satisfied: matplotlib in c:\users\bigza\onedrive\documents\anaco
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Requirement already satisfied: fonttools>=4.22.0 in c:\users\bigza\onedrive\document
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\anaconda\lib\site-packages (from matplotlib) (3.0.9)
Requirement already satisfied: six>=1.5 in c:\users\bigza\onedrive\documents\anacond
a\lib\site-packages (from python-dateutil>=2.8.2->pandas) (1.16.0)
```

Out[2]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunc
0	6	148	72	35	0	33.6	0
1	1	85	66	29	0	26.6	0
2	8	183	64	0	0	23.3	0
3	1	89	66	23	94	28.1	0
4	0	137	40	35	168	43.1	2

Next, We make a list of variables that can not have 0's. Replace them with NA's and count how many invalid numbers we have in each Variable and then we drop all of those valuse and double check our new cleaned data set.

In [3]:
```
col_inval_zero = ['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI']
df[col_inval_zero] = df[col_inval_zero].replace(0 , np.nan)
df.isnull().sum()
```

Out[3]:
```
Pregnancies                 0
Glucose                     5
BloodPressure              35
SkinThickness             227
Insulin                   374
BMI                        11
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

In [4]:
```
df_clean = df.dropna()
df_clean.isnull().sum()
```

Out[4]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

We then get a statistical overview of all numerical values.

In [5]:
```
df_clean.describe()
```

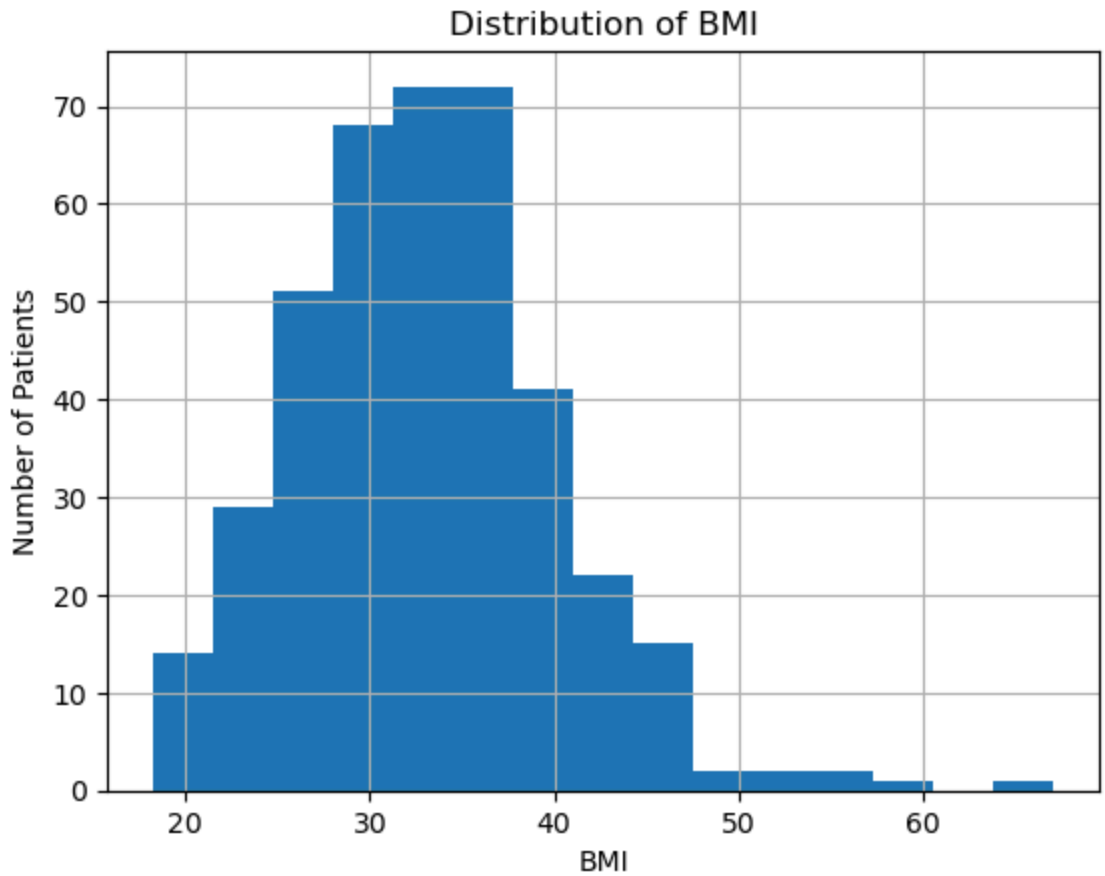
Out[5]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	Dia
count	392.000000	392.000000	392.000000	392.000000	392.000000	392.000000	
mean	3.301020	122.627551	70.663265	29.145408	156.056122	33.086224	
std	3.211424	30.860781	12.496092	10.516424	118.841690	7.027659	
min	0.000000	56.000000	24.000000	7.000000	14.000000	18.200000	
25%	1.000000	99.000000	62.000000	21.000000	76.750000	28.400000	
50%	2.000000	119.000000	70.000000	29.000000	125.500000	33.200000	
75%	5.000000	143.000000	78.000000	37.000000	190.000000	37.100000	
max	17.000000	198.000000	110.000000	63.000000	846.000000	67.100000	

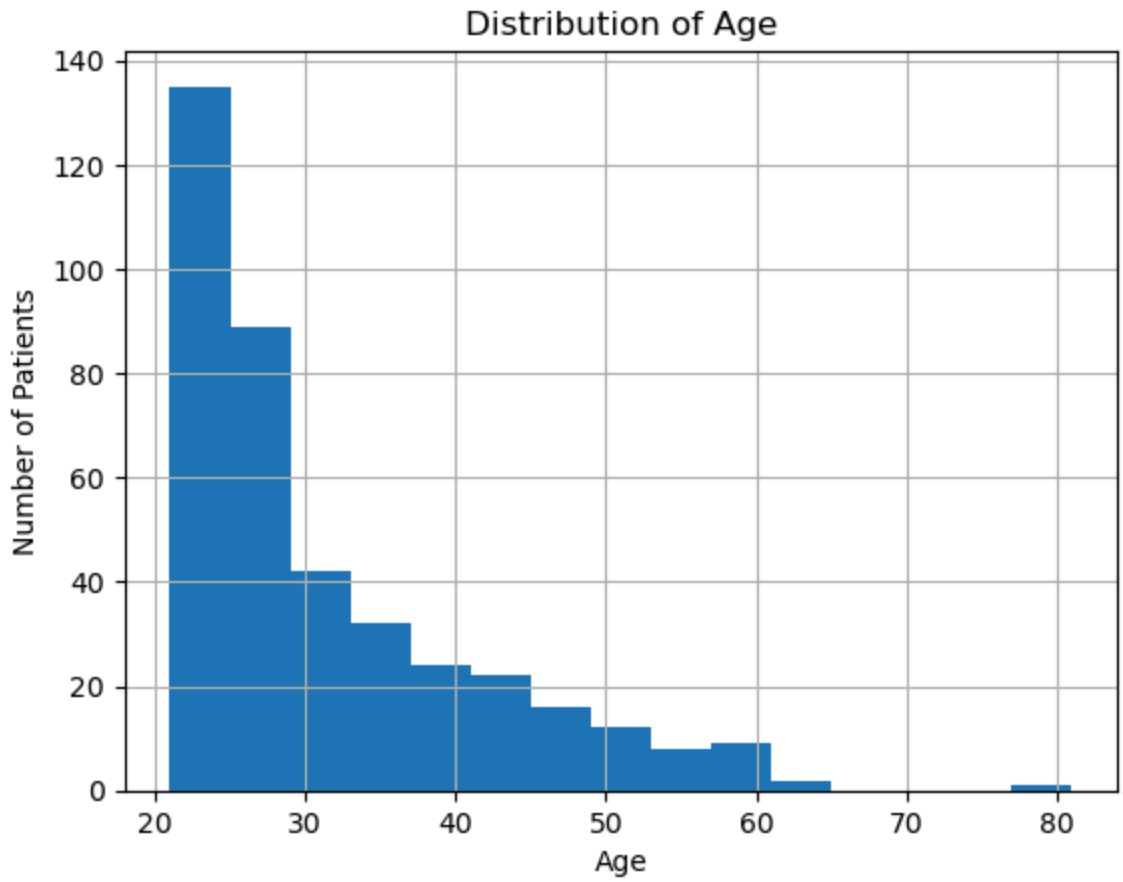
We then make Histograms to show the distibution of BMI , Age , and Glucose Levels. BMI and Glucose Levels show a reliviely Normal distributuon pattern with with some out liers that slightly skew the data. While the Age Histogram is showing highly skewed to the left meaning most of the participants are younger in age.

In [6]:

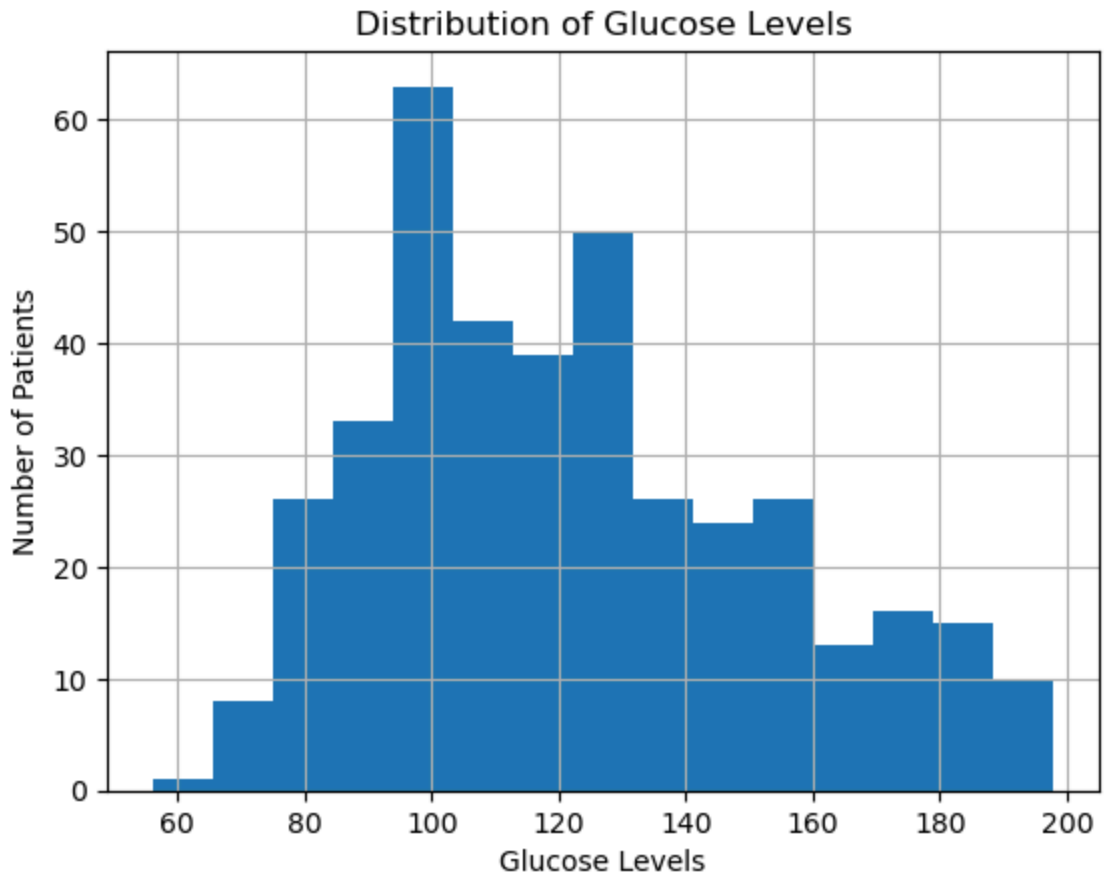
```
df_clean['BMI'].hist(bins = 15)
plt.xlabel("BMI")                # x-axis label
plt.ylabel("Number of Patients")  # y-axis label
plt.title("Distribution of BMI")  # plot title
plt.show()
```



In [7]:
```
df_clean['Age'].hist(bins = 15)
plt.xlabel("Age")                # x-axis label
plt.ylabel("Number of Patients")  # y-axis label
plt.title("Distribution of Age")  # plot title
plt.show()
```



In [8]:
```
df_clean['Glucose'].hist( bins = 15)
plt.xlabel("Glucose Levels")                # x-axis label
plt.ylabel("Number of Patients")  # y-axis label
plt.title("Distribution of Glucose Levels")  # plot title
plt.show()
```



Then we create 2 subsets of groups of diabetics and non diabetics and compare the avg BMI of both groups. This shows that The AVg BMI of NOn Diabetics is lower. We then visually show the distribution of the 2 subsets with the diabetic group showing a normal distributuion pattern and the non diabetic skewing to the left slightly showing that a majority of non diabetics have a lower BMI to their Diabetic counter parts.

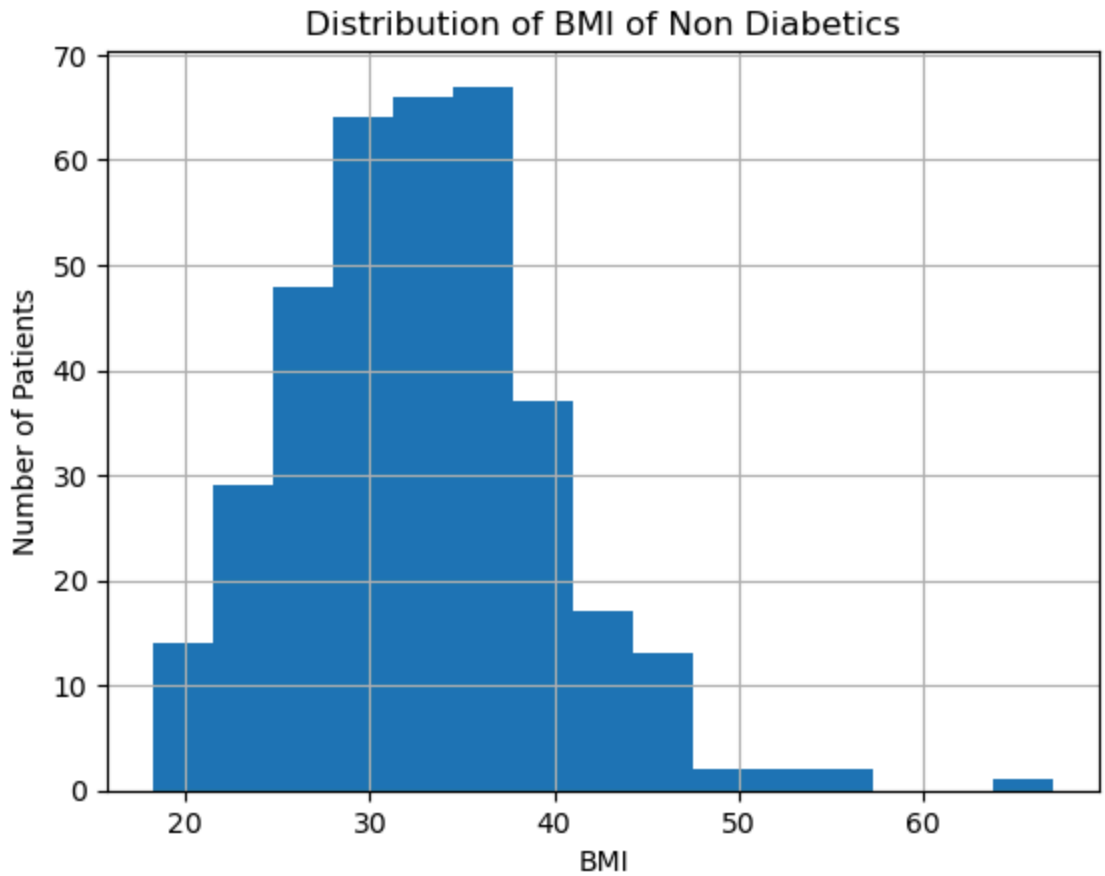
In [9]:
```
df_diabetics = df_clean[df_clean['DiabetesPedigreeFunction'] >= 1]
df_non_diabetics = df_clean[df_clean['DiabetesPedigreeFunction'] < 1]
print("The Average BMI of the Dataset is " + str(df_clean['BMI'].mean()))
```

```
The Average BMI of the Dataset is 33.08622448979592
```

In [10]:
```
print("The Average BMI of Non Diabetics in the Dataset is " + str(df_non_diabetics[
```

```
The Average BMI of Non Diabetics in the Dataset is 32.76988950276243
```

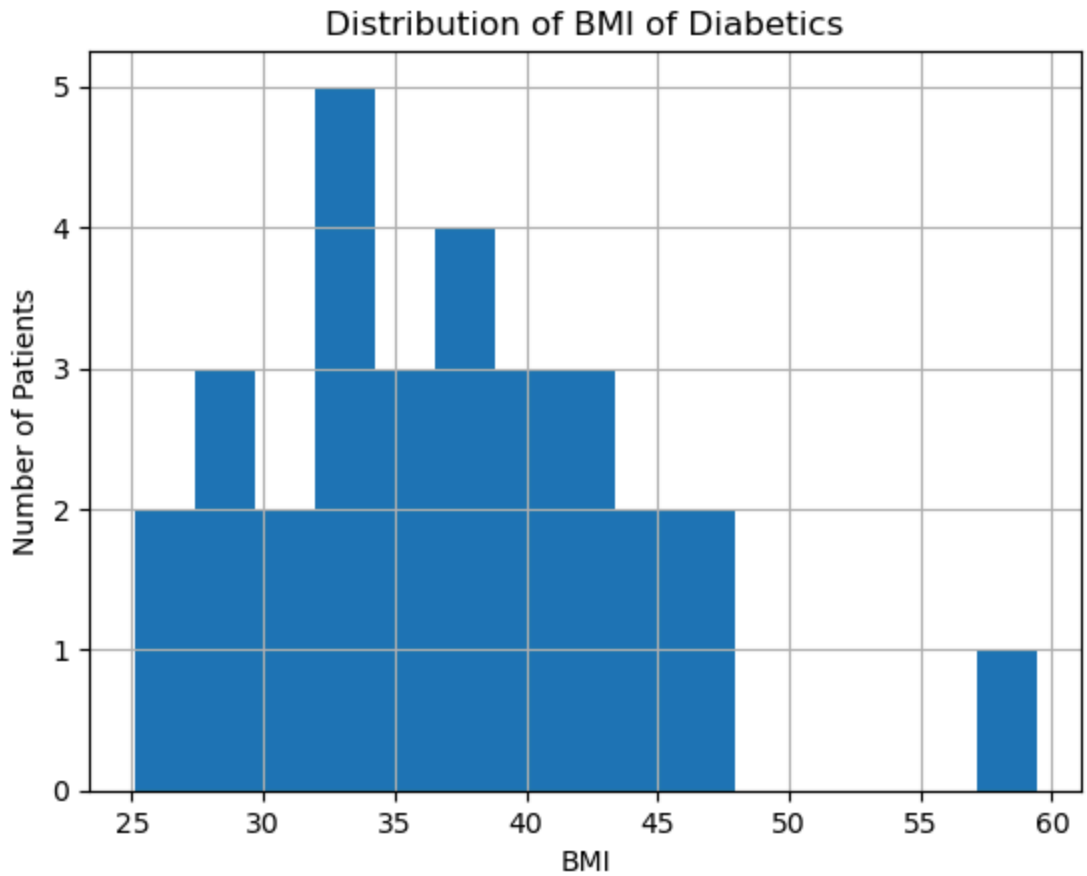
In [11]:
```
df_non_diabetics['BMI'].hist(bins = 15)
plt.xlabel("BMI")                # x-axis label
plt.ylabel("Number of Patients")  # y-axis label
plt.title("Distribution of BMI of Non Diabetics")  # plot title
plt.show()
```



In [12]:
```
df_diabetics['BMI'].mean()
```

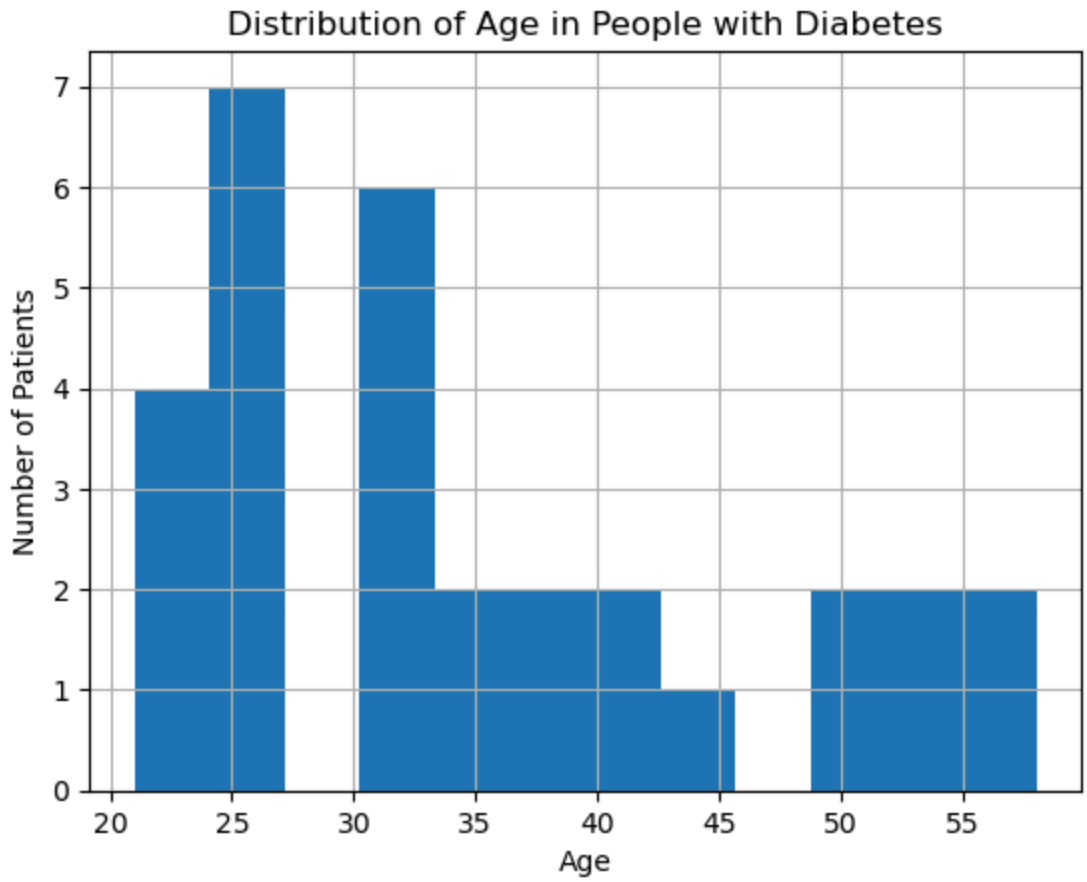
Out[12]: 36.90333333333333

In [13]:
```
df_diabetics['BMI'].hist(bins = 15)
plt.xlabel("BMI")                # x-axis label
plt.ylabel("Number of Patients")  # y-axis label
plt.title("Distribution of BMI of Diabetics")  # plot title
plt.show()
```

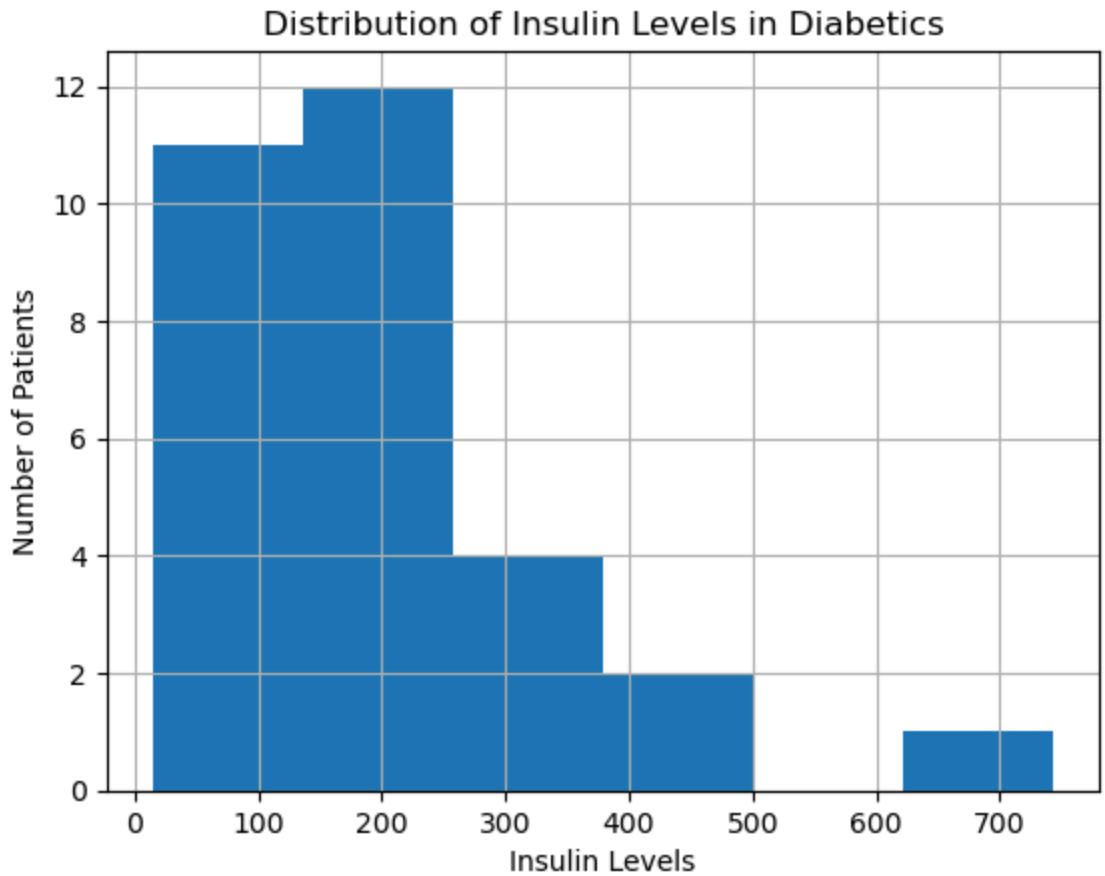


The Next Visuals Show the Distribution of Age in People with Diabetes, Distribution of Insulin Levels in Diabetics, and a Boxplot comparing the BMI of Diabetic vs Non Diabetic.

In [14]:
```
df_diabetics['Age'].hist(bins = 12)
plt.xlabel("Age")                # x-axis label
plt.ylabel("Number of Patients")  # y-axis label
plt.title("Distribution of Age in People with Diabetes")  # plot title
plt.show()
```

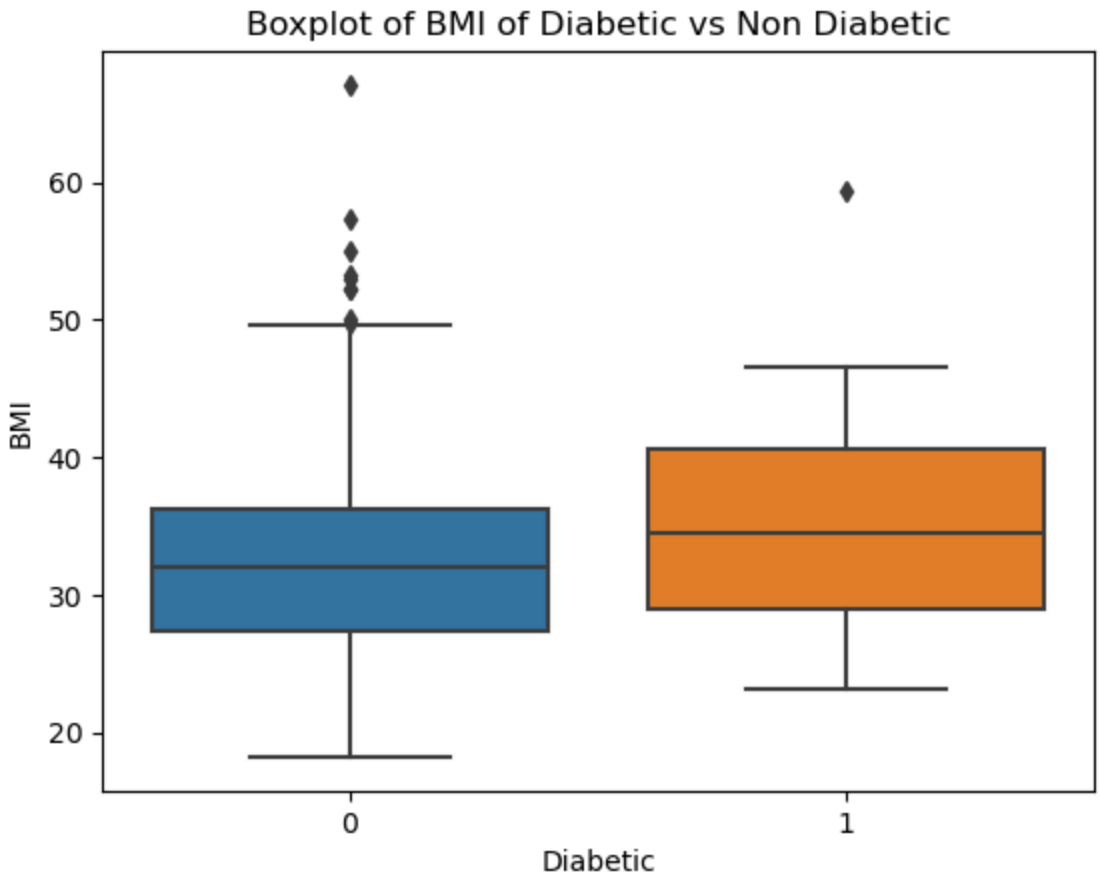


In [15]:
```
df_diabetics['Insulin'].hist(bins = 6)
plt.xlabel("Insulin Levels")                # x-axis label
plt.ylabel("Number of Patients")  # y-axis label
plt.title("Distribution of Insulin Levels in Diabetics")  # plot title
plt.show()
```



In [16]:
```
df["Diabetic"]= np.where(df['DiabetesPedigreeFunction'] >= 1,1,0)
```

In [17]:
```
sns.boxplot(x="Diabetic", y="BMI", data=df)
plt.title("Boxplot of BMI of Diabetic vs Non Diabetic")
plt.show()
```

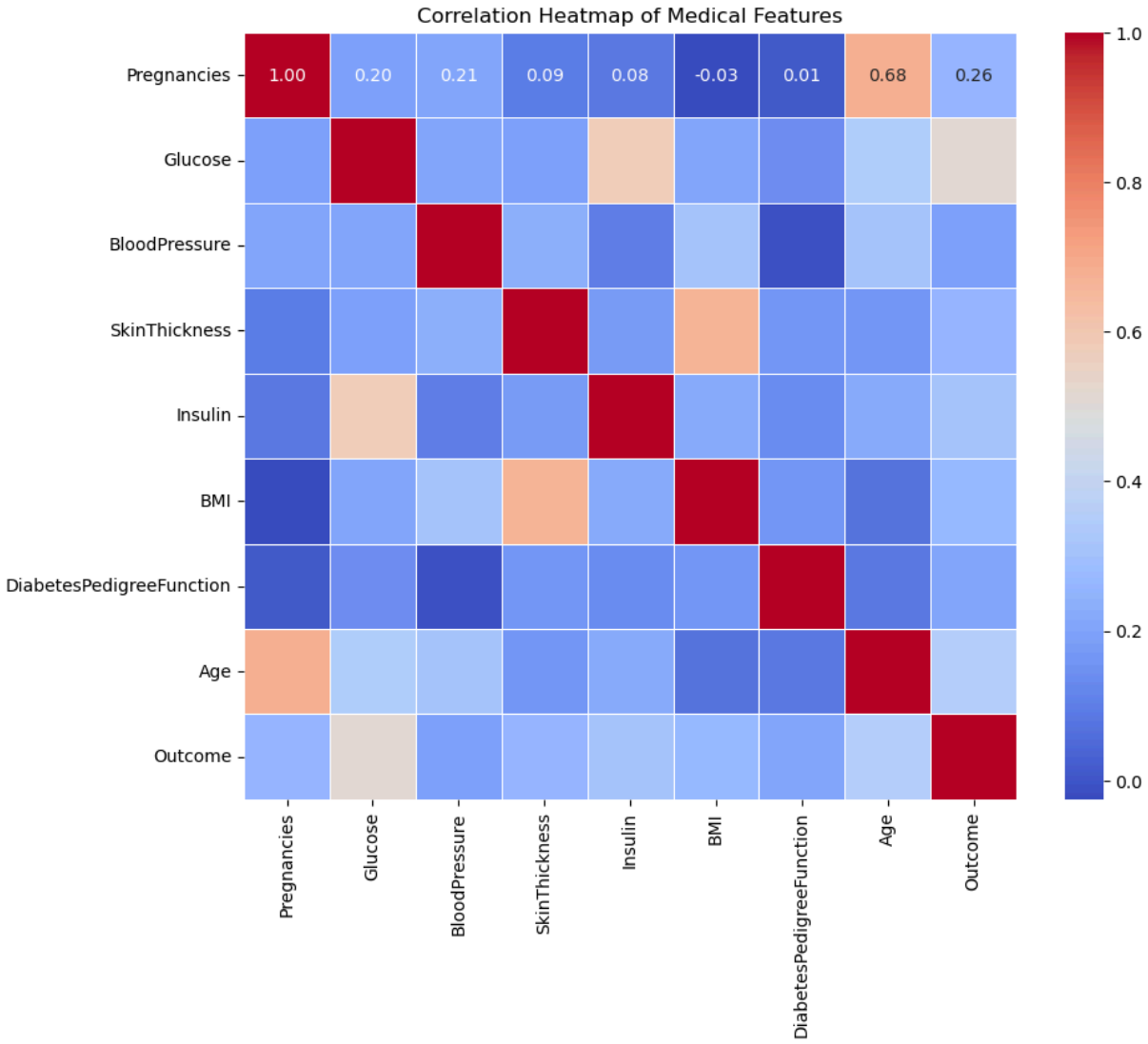


Lastly, we ran a correlation function of all numerical values in the data set showing the more red the square the greater the correlation.

In [19]:
```
corr = df_clean.corr(numeric_only=True)

plt.figure(figsize=(10, 8))
sns.heatmap(corr, annot=True, cmap="coolwarm", fmt=".2f", linewidths=0.5)


plt.title("Correlation Heatmap of Medical Features")
plt.show()
```



This project analyzed clinical health data to explore risk factors associated with the likelihood of developing diabetes. Using data cleaning techniques, we addressed invalid entries in critical health metrics such as glucose, blood pressure, and BMI by replacing biologically impossible zero values with missing indicators and removing incomplete records. Through exploratory data analysis and visualization: BMI, Glucose, and Age were found to have the strongest positive correlation with diabetes outcome. Patients with a Diabetes Pedigree Function ≥ 1 showed higher average BMI values, suggesting a potential compounding effect of genetic risk and lifestyle. The heatmap revealed that Glucose levels had the highest correlation with diabetes presence, aligning with known medical indicatrs.